Tue Jan

8 08:24:01 2002

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_funden:*
5: sp_funden:*
6: sp_mammal:*
7: sp_mammal:*
9: sp_organelle:*
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vartebrate:*
14: sp_unclassified:*
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295
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                                                                                                                                                                                                                                                                                                                                                                                                                                   473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PEQLASAGFYYYGRNDDYKC.....CWESGDDPWYEHAKWFPRCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
sp_organelle:*
sp_phant:*
sp_plant:*
sp_varus:*
sp_varus:*
sp_varus:*
sp_varus:*
                                                                                                                                                                                                                                                                                                                                                                                                  473505
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	17	16	15	14	13	12	11	10	9	8	7	6	ر.	4	ω	N	→	Result No.
174	186	186	188	189	192	195	195	198	209	271	275	277	277	282	290	290	290	Score
59.0	63.1	63.1	63.7	64.1	65.1	66.1	66.1	67.1	70.8	91.9	93.2	93.9	93.9	95.6	98.3	98.3	98.3	Query
496	1 1 1 1 1 1	276	377	379	281	298	280	264	224	324	602	589	589	1140	610	197	195	Length
11	12	12	G	G	12	4	4	12	1	13	11	11	11	4	13	13	13	DB
Q9ESF0	Q9J827	089744	Q9NJ07	Q9U492	Q9YNL8	Q9H2A8	Q9HAP7	Q9EN27	088642	Q9DDN2	Q9ESE9	Q9ESE8	Q9QZC6	Q9UNH1	057319	Q9IA69	Q91A70	Ħ
Qyrois mus muscuiu Q9esf0 rattus norv	Q9j827 spodoptera	089744 buzura supp	Q9nj07 spodoptera	Q9u492 trichoplusi	Q9yn18 choristoneu	. Q9h2a8 homo sapien	Q9hap7 homo sapien	Q9en27 amsacta moo	O88642 rattus norv	Q9ddn2 gallus gall	Q9ese9 rattus norv	Q9ese8 rattus norv	Q9qzc6 rattus norv	Q9unh1 homo sapien	057319 gallus gall	Q9ia69 gallus gall	Q9ia70 gallus gall	Description

ALIGNMENTS

RESULT Q91A69	g Qy	X D O	SO	3 R R	밁	DR DR	RE Z	RT	₽ R	R R N	Š (88	8 8	BE	i i	ij	AC Z	RESULT
ULT 2 A69	1 PEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFDRCE 48	Query Match 98.3%; Score 290; DB 13; Length 195; Best Local Similarity 95.8%; Pred. No. 6.2e-30; Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	NON_TER 195 195 NON_TER 195 AA; 22347 MW; 9C39BFA755E24E48 CRC54;	; PS012 ; PS501	Pfam; PF00653; BIR; 2. SMART; SM00238; BIR; 2.	EMBL; AF221082; AAF35319.1; InterPro; IPR001370; BIR.	Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.	"Genetic variation among chicken lines and mammalian species in	STRAIN-BREED LEGHORN; TISSUE-SPLEEN; Zhou H., Lamont S.J.;	SEQUENCE FROM N.A.	NCBI_TaxID=9031;	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	Galius galius (Chicken). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	INHIBITOR OF APOPTOSIS 1 (FRAGMENT).	01-001-2000 (TIEMBLIE1. 13, Last sequence update) 01-JUN-2001 (TIEMBLIE1. 17, Last annotation update)	2000 (TrEMBLrel. 15, Crea	Q91A70 PRELIMINARY; PRT; 195 AA. Q91A70;	1

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FINGER

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P SEQUENCE FROM N.A.

C STRAIN-BREED FAYOUMI; TISSUE-SPLEEN;
C STRAIN-BREED FAYOUMI; TISSUE-SPLEEN;
A Zhou H., Lamont S.J.;

"Genetic variation among chicken lines and mammalian specie specific genes.";
L Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF721083; AAF33320.1; -.

SUBMITTE FOOTOS; BIR: BIR.

R EMBL; BIR: 2.

SMART; SMO0238; BIR: 2.

SMART; SMO0238; BIR: 2.

PROSITE: PS01282; BIR_REPEAT_1; 2.

PROSITE: PS01281; BIR_REPEAT_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11/HIBITOR OF APOPTOSIS 1 (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Reognathae; Gailiformes; Phasianidae; Phasianinae;
111
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1NHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-WHITE LEGHON; TISSUE-EMBRYONIC FIBROBLAST;

MEDLINE-89038001; PubMed-9372964;

YOU M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;

"ch-lAP1, a member of the inhibitor-of-apoptosis protein family, is medlator of the anniapoptotic activity of the v-rel oncoprotein.";

medlator of the anniapoptotic activity of the v-rel oncoprotein.";

Mol. Cell. Biol. 17:7328-7341(1997).

-1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
*~~h^annia: Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              057319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELLS.
SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE V-REL-TRANSFORMED CELLS.
TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH SPLEEN, TYMMUS, DURSA, INTESTINE, AND LUNG, AND A IN TESTIS, BHAIN, AND SKELETAL MUSCLE.
INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRAN
           PROCESS.

DOMAIN: THE RING FINGER IS IMPORTANT FOR SIMILARITY: MEMBER OF THE IAP FAMILY.

SIMILARITY: CONTAINS 3 BIR DOMAINS (BACUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 98.3%; Similarity 95.8%; 46; Conservative
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197
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Pred. No. 6.3e-30;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                  (BACULOVIRAL
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                                                                                ANTIAPOPTOTIC
                                                                                                                                       TRANSFORMATION
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                  INHIBITION
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                                                                                                                                                                                                                                                                                                                                                                        V-REL-TRANSFORMED
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                                                                                                                                                                                                                                                                                                     CYTOPLASM OF
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       RESULUTION OF THE PRICE OF THE 
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Best Local S
Matches 46
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-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FI
EMBL; AF008592; AAB8044.1; -.
HSSP, Q13490; 1QBH.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD; 1.
Pfam; PF00653; BIR; 3.
Pfam; PF00097; Zf-C3H44; 1.
SMART; SM00134; CARD; 1.
SMART; SM00134; CARD; 1.
SMART; SM00134; CARD; 1.
SMART; SM00134; CARD; 1.
SMART; SM00134; ST-C3H44; 1.
SMART; SM00134; ST-C3H47; 3.
PR0SITE; PS01382; BIR, REPEAT_2; 3.
PROSITE; PS01383; BIR, REPEAT_2; 3.
PROSITE; PS01383; BIR, REPEAT_2; 3.
PROSITE; PS0139; CARD; 1.
EMBL; AF123094; AAD46161.1; --
HSSF; 013490; 108H.
InterPro; IPR001370; BIR
InterPro; IPR001370; ICE_P20.
InterPro; IPR001309; ICE_P20.
InterPro; IPR001309; IGE_P20.
InterPro; IPR003500; Ig_like.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00653; BIR; 3.
SMART; SM00218; BIR; 3.
SMART; SM00115; CASC; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSUNHI PRELIMINARY;
OSUNHI PRELIMINARY;
OSUNHI:
OSUNHI:
OSUNHI PROBLECTION (TEMBLECT 13, LOSUNHI PROSION PROTEIN.
APIZ-MLT FUSION PROTEIN.
APIZ-MLT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE-99272400; PubMed-10339464;

MEDILINE-99272400; PubMed-10339464;

MEDILINE-99272400; PubMed-10339464;

MEDILINE-99272400; PubMed-10339464;

MEDILINE-90272400; PubMed-10339464;

MEDILINE-902724000; PubMed-10339464;

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REPEAT
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis;
REPEAT
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30 97 BIR REPEAT
176 242 BIR REPEAT
262 329 BIR REPEAT
263 329 C3HC4-TYPE.
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176
262
563
510 AA;
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329 B
597 C
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Last annotation update)
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Pred. No. 2e-29;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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610; 0; Gaps

327 48

CRC64; Length Indels

RESULT 057319

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Дb Š

135

Matches

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FROM N.A.

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Best Local S
Matches 45
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Best Local S
Matches 44
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InterPro; IPRO01315; CARD.
InterPro; IPR001841; 2nf_ring.
InterPro; IPR001841; 2nf_ring.
InterPro; IPR001841; 2nf_ring.
InterPro; IPR001841; 3.

Pfam; PF00653; BIR; 3.

Pfam; PF00697; zf-C3HC4; 1.

Pfam; PF00097; zf-C3HC4; 1.

SMART; SM002184; CARD; 1.

SMART; SM00184; RING; 1.

SMART; SM00184; RING; 1.

SMART; SM00182; BIR_REPEAT_1; 3.

PROSITE; PS01282; BIR_REPEAT_2; 3.

PROSITE; PS0129; CARD; 1.
                                                                                                                                                          Q9ESE8 PRELIMINARY; PRT; 589 AA.
Q9ESE8;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QZC6 PRELIMINARY; PAL; JOJ.....
Q9QZC6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLEL 17, Last annotation
INHIBITOR OF APOPTOSIS PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M. "Cloning of cDNA for rat inhibitor of apoptosis protein 2. Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. EMBL; AF190020; AAF04585.1; -. EMBL; AF190020; AAF04585.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                           Rattus norvegisus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat

MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDDWVEHAKWFPRCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQHAKWFPRCE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50143;
PS50208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIR_REPEAT_2; 3.
CASPASE_P20; 1.
a; 128738 mw; 0C18D890287C723E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 282; DB
Pred. No. 4.2e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 277; DB 11;
Pred. No. 9.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E6812FFE3EA34142
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.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 589;
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                                                                           Rattus
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Query Match
Best Local 5
Matches 43
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Apoptosis Protein 1, 2, and 3 Genes.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
C --- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
REMBL; AF183431; AAG22971.1; -.
InterPro; IPR001315; CARD.
RE InterPro; IPR001315; CARD.
RE InterPro; IPR001841; Znf_ring.
RP Ffam; PF00653; BIR; 3.
RP Ffam; PF00653; BIR; 3.
RP Ffam; PF00679; zf-C3HC4; 1.
RR Pfam; PF00679; zf-C3HC4; 1.
RR SMART; SM00134; CARD. 1.
RR SMART; SM00134; CARD. 1.
RR SMART; SM00134; RING; 1.
RR PROSITE; PS01282; BIR_REPEAT_1; 1.
RR PROSITE; PS50143; BIR_REPEAT_1; 1.
RR PROSITE; PS50143; BIR_REPEAT_2; 3.
RR PROSITE; PS50143; BIR_REPEAT_1; 1.
RR PROSITE; PS50144; BIR PART PROSITE; PS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 44; Conser
                                                                                                                                                                                             Pfam; PF00653; BIR; 3.
Pfam; PF00069; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 1
PROSITE; PS05143; BIR_REPEAT_2; 3
PROSITE; PS050143; BIR_REPEAT_2; 3
PROSITE; PS050143; BIR_REPEAT_2; 3
PROSITE; PS050143; BIR_REPEAT_2; 3
PROSITE; PS05019; CARD; 1.
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Holcik M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and Characterization of the Rat Homologs of the Apoptosis Protein 1, 2, and 3 Genes.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
EMBL; AF188430; AA622970.1;
InterPro; IPR001370; BIR.
InterPro; IPR001371; CARD.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9ESE9 PRELIMINARY; PRT; 602 AA.

O9ESE9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11-HIBITOR OF APOPTOSIS PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holcik M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEQLASAGFYYYDHNDDVKCFCCDGGLRCWEPGDDPWIEHAKWFPRCE 306
       1 Similarity
43; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lefebvre C.A., Hicks K.,
                                                                                                                                                                           602
       Conservative
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                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66750
                                                                                                                                                                           67326
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                                    93.2%;
                                                                                                                                                                           M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 277; DE Pred. No. 9.4e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
       ω
--
                                    Score 275;
Pred. No. 1
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B4F7089BD7CD285B
                                                                                                                                                                           CC91385EEA62DE5A CRC64;
   Mismatches
                                                                                                                                                                                                                                                                          ω μ
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e_Rat Homologs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 589;
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       Indels
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                         602;
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   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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       Gaps
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QY

PEQLASAGEYYYGRNDDYKCFCCDGGLRCWESGDDPWVEHAKWFPRCE 48

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OPEDIN
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            SQ PTT RACE TO DESCRIPTION OF THE PROPERTY OF 
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Best Local S
Matches 43
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P PENGLECTOR C.N., Bargmann W.J., Varadarajan J., Bose H.R. J

T "The apoptosis inhibitor ch-IAPl is a direct transcription

T v-Rel and c-Rel.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

E EMBL, AF311289; AAG42316.1; -.

R InterPro; IPR001370; BIR.

R InterPro; IPR001370; BIR.

R PF00153; BIR; 3.

R SMART; SM00238; BIR; 3.

R PROSITE; PS00138; BIR_REPEAT_1; 1.

R PROSITE; PS0113; BIR_REPEAT_2; 3.

R NONTER 324 324
                                                                                                                                                                                                                    "Cloning and characterisation of an inhibitor of apoptosis (IAP) in the rat corpus luteum.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases EMBL;

H5SP; Q11490; 1QBH,

InterPro; IPBAA***
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O9DDN2

O9DDN2;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation updat)
APOPTOSIS INHIBITOR CH-IAPO1 (FRAGMENT).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Gallus Gallus (Chicken).
Gallus Gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              088642 PRELIMINARY; PRT; 224 AA. 088642; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 10, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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        NON_TER
SEQUENCE
                                                                                                            Interpro; IPRO01370; BIR.
Interpro; IPRO01370; BIR.
Pfam; PO0653; BIR; 2.
SMART; SM00238; BIR; 2.
PROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INHIBITOR OF
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43; Conservative
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224
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8A;
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95.6%;
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1; Mis
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Sciurognathi; Muridae;
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Pl is a direct transcriptional target
        213A52534D5EB56A CRC64;
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; Murinae; Rat
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Best Local S
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Best Local
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                                                                                                                                          EMBL; AF250284; AAG02727.1; -.
InterPro: IFR001370; BIR.
InterPro: IFR001841; Znf_ring.
InterPro: IFR001841; Znf_ring.
Pfam; PF00653; BIR; 2.
SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; PS50143; BIR_REPEAT_2; 2
SEQUENCE 264 AA; 30547 MW; 2E
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Q9EN27;
Q1-MAR-2001
01-MAR-2001
01-JUN-2001
  J. Biol. Chem. 0:0-0(2000)
                   SEQUENCE FROM N.A.
Kasof G.M., Gomes B.C.;
"Livin, a novel inhibitor-of-apoptosis
                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete Genomic Sequence of the Amsacta moorei Analysis and Comparison with Other Poxviruses."; Virology 274:120-139(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=20396580;
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Entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMV021
                                                                                                 NCBI_TaxID-9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moyer R.W.;
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sberg K.J., Diggans
                                                                                                                    Chordata;
Primates;
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61.78;
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Last annotation updat
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Pred. No. 2.2e-19;
                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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2EB72DA4B58D920A CRC64;
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InterPro: IPR001841; Znf_ring.
Pfam; PF00653; BIR; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00238; BIR; 1.
SMART; SM00184; RING; 1.
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SEQUENCE FROM N.A.
Ashhab Y., Alian A., Polliack A., Panet A., Ben-Yehuda D.;
Ashhab Y. Alian A., Polliack A., Panet A., Ben-Yehuda D.;
"Two splicing variants of a new inhibitor of apoptosis gene with
"Two splicing variants of a new inhibitor of apoptosis gene with
different biological properties and tissue distribution pattern.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9H2A8 PRELIMINARY; PRT; 298 AA.
09H2A8; O1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1NHIBITOR OF APOPTOSIS FOTEIN KIAP (BAZGINI1.1.2) (BACULOVIRAL REPEAT-CONTAINING PROTEIN 7 (LIVIN), ISOFORM 2).
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"Two splicing variants of a new inhibitor of apoptosis gene with
different biological properties and tissue distribution pattern.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-KINEY;
Lin J. H., Deng G., Huang Q., Morser J.;
A Novel member of the inhibitor of apoptosis
Res. Commun. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCHI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50143; BIR_REPEAT_2; 1.

PROSITE; PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1.

Zinc-finger.
                                                                  -i- SIMILARITY: CONTAINS A RING-TYPE EMBL; AF301009; AAG37878.1; -. EMBL; AJ309298; CAC37338.1; -. EMBL; AL121827; CAC36111.1; -. InterPro; IPR001370; BIR. InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
Alian !
                                                                                                                                                                                                                                                                                                                Submitted (APR-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Conservative
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A RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 195; DB Pred. No. 1.8e 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                               ZINC FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
.8e-17;
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Best Local
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InterPro; IPR001841; Znf_ring.
Pfam; PP00653; BIR; 2.
Pfam; PP00907; zf-C3HC4; 1.
SMART; SM00238; BIR; 2.
SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; UPROSITE; PS01282; BIR_REPEAT_2; 2.
Zinc-finger.
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Q9YNL8;
Q1-MAY-1999
Q1-MAY-1999
Q1-JUN-2001
                                                                                                                                                                                                                                                           Q9U492;
Q9U492;
01-MAY-2000
01-MAY-2000
01-JUN-2001
IAP1.
Trichoplusia ni (Cabbage looper).
Trichoplusia ni (Cabbage looper).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Noctuoldea; Noctuidae; Plusiinae; Trichoplusia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00238; BIR; 1.
SMART; SM00184; RING; 1.
PROSITE; PS50143; BIR_REPEAT_2; 1.
PROSITE: PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1
Zinc-finger.
SEQUENCE 298 AA; 32798 MW; B2EAAEE531BEC10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U82510; AAD00537.1;
HSSP; Q13490; 1QBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleopolyhedrovirus.
NCBI_TaxID-10448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choristoneura fumiferana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CfMNPV IAP gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lauzon H., Arif B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 PELLAAAGFFHTGHQDKVRCFFCYGGLQSWKRGDDPWTEHAKWFPSCQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 PEKLAEAGFFYTGRSDKVKCFYCDGGLDNWEQDDEPWQQHALWFGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 30; Conserv
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31; Conservative
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)F APOPTOSIS PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.1%;
66.0%;
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62.5%;
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                                                                                                                                                                                                                              PROTEIN.
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no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 192; DB 12;
Pred. No. 4.5e~17;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B2D9BE8A359F105E CRC64;
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annotation
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.9e-17;
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RESULT 15
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SEQUENCE FROM N.A.

( MEDLINE-20062908; PubMed-10593985;

X Seshagiri S., Vucic D., Lee J., Dixit V.M.;

Y Seshagiri S., Vucic D., Lee J., Dixit V.M.;

"Baculovirus-based genetic screen for antiapop

T novel IAP.";

J. Biol. Chem. 274:36769-36773(1999).

EMBL, AF195528; AAF19819.1; ~.

R MSSP; Q13490; 108H.

R HSSP; Q13490; 108H.

R InterPro; IPR001370; BIR,

R InterPro; IPR001370; BIR,

R InterPro; IPR001370; BIR,

DR Pfam; PF00653; BIR; 2.

DR SMART; SM00128; BIR; 2.

DR SMART; SM00128; BIR; 1.

DR PROSITE; PS0128; BIR, REPEAT_1; UNKNOWN_2.

DR PROSITE; PS01283; BIR_REPEAT_2; 2.

SO SEQUENCE 379 AA; 41857 MW; 069381A012D9DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OX DR RT DR 
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mammalian caspase-9.";

Proc. Natl. Acad. Sci. U.S.A. 97:1427-1432(2000).

REMBL: AF186378; AAF35285.1;

RINTERPRO: IPR001370; BIR.
InterPro: IPR001841; Znf_ring.
REMBL: SEP00653; BIR; 2.
SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1.
REMORT: SM00184; RING; 1.
REMORT: PS0128; BIR; 2.
REMORT: SM00184; RING; 1.
REMORT: PS0128; BIR; 2.
REMORT: PS0128; BIR, REPEAT_1; UNKNOWN_2.
REMORT: PS0143; BIR, REPEAT_2; 2.
REMORT: PS0143; BIR; REMORT: PS0143; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.18;
Best Local Similarity 61.78;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDILINE-20144055; PubMed-10677478;

Huang Q., Deveraux Q.L., Maeda S., Salvesen G.S., Stennicke H.R.,

Hammock B.D., Reed J.C.;

"Evolutionary conservation of apoptosis mechanisms: Lepidopteran

baculoviral inhibitor of apoptosis proteins are inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
NCBI_TaxID=7108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9NJ07 PRELIMINARY; PRT; 377 AA.
Q9NJ07;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7111;
[1]
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PEELAEAGFFYTGQGDKTKCFYCDGGLKDWENHDVPWEQHARWFDRC 274
                                                 PEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRC 47
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                           63.7%;
                                                                                                                                                                                                             Score 188; DB 5; Length 377; Pred. No. 2e-16; 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 189; DB 5; L
Pred. No. 1.5e-16;
7; Mismatches .11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F1207D2D3ED60B3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     069381A012D9DE65 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                         Gaps
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Search completed: January 7, 2002, 16:03:54 Job time: 1413 sec

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